AMENDMENTS TO THE CLAIMS

Please enter the following amendments without prejudice or disclaimer.

Please cancel claims 22-34 without prejudice or disclaimer.

This listing of claims will replace all prior versions, and listings, of claims in the application:

Claim 1 (Original): A method for generating a *Drosophila* clipped *FRT* (cFRT) chromosome insensitive to a *P* transposase but remaining functional to a yeast site-specific flippase recombinase (FLP), comprising steps of:

(a) exposing a *FRT* chromosome to said *P* transposase for occurring a local and imprecise transposition, wherein said *FRT* chromosome contains a *P*[*FRT*] insertion with a selection marker gene;

(b) screening said *P[FRT]* insertion insensitive to said *P* transposase to obtain screened products;

(c) selecting candidate products from said screened products by further examinations; and

(d) exposing said candidate products by said *P* transposase and selecting a desired product by said further examinations to obtain said *Drosophila* clipped *FRT* (cFRT) chromosome is insensitive to said *P* transposase but remaining functional to yeast site-specific flippase recombinase.

Claim 2 (Original): The method according to claim 1, wherein said method further comprises a step (e) of examining the actual molecular nature of said clipped insertion by PCR (polymerase chain reaction).

Claim 3 (Original): The method according to claim 1, wherein said step (c) further comprises steps of:

(c1) examining said screened products for both recombination capability and homozygous viability; and

(c2) examining recombination accessibility of FRT sequences contained in a clipped *P[FRT]* insertion by the presence of said FLP to obtain said candidate products.

Claim 4 (Original): The method according to claim 3, wherein said recombination capability represents the functional activity of said clipped *P[FRT]* insertion and its homologous location relative to that of said original *P[FRT]* insertion.

Claim 5 (Original): The method according to claim 3, wherein said homozygous viability represents a genetic background after said chromosome's exposure to said *P* transposase.

Claim 6 (Original): The method according to claim 1, wherein said step (d) of exposing said candidate products by said *P* transposase and selecting said desired product by said further examinations is repeated at least twice.

Claim 7 (Original): The method according to claim 1, wherein said *Drosophila* cFRT chromosome is an isogenized homozygous viable *Drosophila* second chromosome.

Claim 8 (Original): The method according to claim 1, wherein said cFRT is formed due to a target sequence, recognized by said *P* transposase and responsible for a *P* transposase transposition, which is damaged and alternated into a type of incomplete target sequence, through one of a group consisting of:

(1) missing of a P5' DNA sequence region;

(2) missing of a P3' DNA sequence region; and

(3) missing of DNA sequences other than those defined in item (1) and in item (2).

Claim 9 (Original): The method according to claim 1, wherein said *Drosophila* cFRT chromosome remains the functional activity of said cFRT insertion for a site-specific recombination in the presence of said FLP.

Claim 10 (Original): The method according to claim 1, wherein an effectiveness of said *Drosophila* cFRT chromosome is monitored by a FLP-FRT system and derived modification systems thereof.

Claim 11 (Original): The method according to claim 1, wherein an effectiveness of said cFRT chromosome is monitored by molecular biology methods for the description of said cFRT DNA sequences configuration.

Claim 12 (Original): The method according to claim 1, wherein said *Drosophila* cFRT chromosome remains to behave normally as a wild type chromosome feasible for various genetic manipulations.

Claim 13 (Original): The method according to claim 1, wherein a clipped *P[FRT]* insertion is alternatively moved to another chromosome from said *Drosophila* clipped *FRT* (cFRT) chromosome by treating said *Drosophila* cFRT chromosome with one of mutagens and X-ray.

Claim 14 (Original): The method according to claim 1, wherein said *Drosophila* cFRT chromosome is alternatively used to establish a *Drosophila* cell line based on a genetic background of said *Drosophila* cFRT chromosome.

Claim 15 (Original): The method according to claim 1, wherein said *Drosophila* cFRT chromosome is mutated to obtain gene mutations for further experiment.

Claim 16 (Original): The method according to claim 15, wherein a molecular information of said gene mutations is recovered by retrieving flanking DNA sequences of a clipped *P[FRT]* insertion with a molecular biology method.

Claim 17 (Original): The method according to claim 16, wherein said molecular biology method includes a plasmid rescue method, a inversed PCR method and a chromosomal walking method.

Claim 18 (Original): The method according to claim 16, wherein said molecular information of said gene mutations can be recovered by a related bioinformatic manipulation.

Claim 19 (Original): The method according to claim 18, wherein said related bioinformatic manipulation includes blasting database, searching gene homologues of biological

organisms, analyzing comparative genomics, and analyzing phylogenic distance and relationship.

Claim 20 (Original): The method according to claim 15, wherein the functional description of said gene mutations are further analyzed based on the information obtained from said molecular biology method and said related bioinformatic manipulation by using a biological technique.

Claim 21 (Original): The method according to claim 1, wherein said *Drosophila* cFRT chromosome is used to study the *Drosophila* genes located on the second chromosome and their corresponding gene homologues of other biological organisms including vertebrates, invertebrates, eukaryotes and prokaryotes.

Claims 22-34 (Canceled)